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(54) Title: SYNTHETIC GENE

ATG GAC CCG TCC AAG GAC TCC AAA GCT CAG GTT TCT GCA GCC GAA GCT GGT ATC ACT GGC ACC TGG TAT AAC CAA CTG GGG TCG ACT TTC ATT GTG ACC GCT GGT GCG GAC GGA GCT CTG ACT GGC ACC TAC GAA TCT GCG GTT GGT AAC GCA GAA TCC CGC TAC GTA CTG ACT GGC CGT TAT GAC TCT GCA CCT GCC ACC GAT GGC TCT GGT ACC GCT CTG GGC TGG ACT GTG GCT TGG AAA AAC AAC TAT CGT AAT GCG CAC AGC GCC ACT ACG TGG TCT GGC CAA (I) TAC GTT GGC GGT GCT GAG GCT CGT ATC AAC ACT CAG TGG CTG TTA ACA TCC GGC ACT ACC GAA GCG AAT GCA TGG AAA TCG ACA CTA GTA GGT CAT GAC ACC TTT ACC AAA GTT AAG CCT TCT GCT GCT AGC ATT GAT GCT GCC AAG AAA GCA GGC GTA AAC AAC GGT AAC CCT CTA GAC GCT GTT CAG CAA TAA

(57) Abstract

Synthetic DNA coding for streptavidin includes sequence (I) and incorporates useful restriction sites at frequent intervals to facilitate the cassette mutagenesis of selected regions. Also included are flanking restriction sites to simplify the incorporation of the gene into any desired expression system.

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SYNTHETIC GENE

This invention relates to synthetic genes coding for streptavidin.

Streptavidin is a 60 kD protein isolated from Streptomyces avidinii that binds extremely tightly to the vitamin biotin with a dissociation constant of about 10⁻¹⁵ M. Streptavidin is composed of four identical subunits of 15 kD and binds 4 mole biotin per mole of protein. It is structurally related to the protein avidin, a biotin binding protein isolated from chicken egg whites.

Streptavidin has particular utility in that it can be readily conjugated to a range of other proteins such as horseradish peroxidase and alkaline phosphatase. This has allowed the development of sensitive detection systems for biotinylated oligonucleotides, antibodies and other binding proteins with application in the analysis of DNA, RNA, protein and carbohydrates.

The natural gene for streptavidin has been described and was found to encode a protein of 183 amino acids which included a typical leader sequence of 24 amino acids. The N-terminus of the mature protein was found to correspond to residue 25 of the deduced sequence. The amino acid sequence of mature streptavidin deduced from the gene sequence was used as the basis of the design for the synthetic streptavidin genes of the present invention and is shown in Figure 1.

The binding of streptavidin to biotin was described in 1963 by Chaiet et al. (Agents Chemother. 3, 28-32). The cloning of the natural streptavidin gene and its sequence together with the deduced streptavidin amino acid sequence is taught by Argarana et al. (Nucleic Acids Res. 14 1871-1882 (1986)). The production of streptavidin-like polypeptides is disclosed in EP-A-0198015 (Biogen NV).

In order to facilitate the dissection of the structure/function relationships of streptavidin, its incorporation into expression vectors and the production of novel chimeric proteins containing streptavidin functionality an improved novel synthetic gene for the streptavidin produced by <u>Streptomyces avidinii</u> is sought.

It is by no means easy to predict the design of an improved streptavidin gene, since the factors that determine the expressibility of a given DNA sequence are still poorly understood. Furthermore, the utility of the gene in various applications will be influenced by such considerations as codon usage and restriction sites. The present invention relates to a synthetic streptavidin gene which is distinct from the natural streptavidin gene and has advantages in the ease with which it can be modified due to the presence of useful restriction sites.

When synthesising and assembling genes, problems have been encountered when there are inverted or direct repeats greater than eight bases long in the genetic sequence. In addition, areas of unbalanced base composition such as G/C or A/T rich regions or polypurine/polypyrimidine tracts have been found to lead to inefficient expression. The present invention seeks to overcome or at least alleviate these difficulties.

According to a first aspect of the invention, there is provided DNA coding for streptavidin and having restriction sites for the following enzymes:

EcoRI, NdeI, PstI, SalI, SacI, SnaBI, BspMI, KpnI, FspI, PflMI, DraIII, BalI, BstXI, HpaI, NsiI, SpeI, NheI, BstEII, XbaI, BamHI and HindIII

According to a second aspect of the invention, there is provided DNA including the following sequence:

A synthetic streptavidin gene as described above incorporates useful restriction sites at frequent intervals to facilitate the cassette mutagenesis of selected regions. Also included are flanking restriction sites to simplify the incorporation of the gene into any desired expression system.

Codons are those that are favoured by $\underline{E.\ coli}$ but it is expected that the DNA would be suitable for expression in other organisms including yeast and mammalian cells.

Certain DNA sequences in accordance with the invention encode the entire mature streptavidin protein together with the required initiator methionine residue but lack the leader sequence present in the natural gene. It is envisaged that the leader sequence appropriate to the expression system of choice would be added to the synthetic gene as required or omitted to allow for intracellular expression of the gene.

According to a third aspect of the invention, there is provided a genetic construct comprising DNA according to the first or second aspect or a fragment thereof. The fragment may comprise at least 10, 20, 30, 40 or 50 nucleotides. A genetic construct in accordance with the third aspect may be a vector, such as a plasmid, cosmid or phage. Alternatively or in addition, a genetic construct in accordance with the third aspect may be a chimeric gene composing all or a fragment of DNA according to the first or second aspect fused to any other sequence of DNA so as to result in a sequence capable of encoding a hybrid protein possessing biotin binding activity.

According to a fourth aspect of the invention, there is provided a process for the preparation of DNA in accordance with the first or second aspect or a genetic construct in accordance with the third aspect, the process comprising coupling successive nucleotides and/or ligating appropriate oligomers.

The invention also relates to other nucleic acid (including RNA) either corresponding to or complementary to DNA in accordance with the first or second aspects.

Preferred embodiments and examples of the invention will now be described. In the following description, reference is made to a number of drawings, in which:

Figure 1 shows the amino acid sequence of streptavidin;

Figure 2 shows a sequence of a streptavidin synthetic gene in accordance with the invention incorporating a summary of restriction sites;

Figure 3 shows a sequence of a synthetic streptavidin gene in accordance with the invention divided into oligonucleotides; and

Figure 4 shows a summary of an assembly procedure used.

EXAMPLE

CONSTRUCTION OF THE GENE

The desired gene sequence was divided into 24

oligodeoxyribonucleotides (oligomers) as depicted in Figure 3. The division was such as to provide 7 base cohesive ends after annealing complementary pairs of oligomers. The end points of the oligomers were chosen to minimise the potential for inappropriate ligation of oligomers at the assembly stage.

The oligomers were synthesised by automated solid phase phosphoramidite chemistry. Following de-blocking and removal from the controlled pore glass support the oligomers were purified on denaturing polyacrylamide gels, further purified by ethanol precipitation and finally dissolved in water prior to estimation of their concentration.

All the oligomers with the exception of the 5' terminal oligomers BB214 and BB237 were then kinased to provide them with a 5' phosphate as required for the ligation step. Complementary oligomers were then annealed and the 12 pairs of oligomers ligated together by T4 DNA ligase as depicted in Figure 4. The ligation products were separated on a 2% low gelling temperature (LGT) gel and the band corresponding to the 501/501 bp streptavidin gene duplex was cut out and extracted from the gel. The purified fragment was ligated to EcoRI/HindIII cut DNA of the plasmid vector pUC18. The ligated product was transformed into HW87 and plated on L-agar plates containing 100 mcg ml⁻¹ ampicillin. Colonies containing potential clones were then grown up in L-broth containing ampicillin at 100 mcg ml^{-1} and plasmid DNA isolated. Positive clones were identified by direct dideoxy sequence analysis of the plasmid DNA using the 17 base universal primer, a reverse

sequencing primer complementary to the opposite strand on the other side of the polylinker and some of the oligomers employed in the assembly of the gene that served as internal primers. One streptavidin clone was subsequently re-sequenced on both strands to confirm that no mutations were present.

METHODS

All the techniques of genetic manipulation used in the manufacture of this gene are well known to those skilled in the art of genetic engineering. A description of most of the techniques can be found in the laboratory manual entitled Molecular Cloning by T. Maniatis, E.F. Fritsch and J. Sambrook published by Cold Spring Harbor Laboratory, Box 100, New York.

Additional and modified methodologies are detailed below.

1) Oligonucleotide synthesis

The oligonucleotides were synthesised by automated phosphoramidite chemistry using cyanoethyl phosphoramidtes. The methodology is now widely used and has been described (Beaucage, S.L. and Caruthers, M.H. Tetrahedron Letters 24, 245 (1981)).

2) Purification of Oligonucleotides

The oligonucleotides were de-protected and removed from the CPG support by incubation in concentrated $\rm NH_3$. Typically, 50 mg of CPG carrying 1 micromole of

oligonucleotide was de-protected by incubation for 5 hr at 70° in 600 mcl of concentrated NH₃. The supernatant was transferred to a fresh tube and the oligomer precipitated with 3 volumes of ethanol. Following centrifugation the pellet was dried and resuspended in 1 ml of water. The concentration of crude oligomer was then determined by measuring the absorbance at 260 nm.

For gel purification 10 absorbance units of the crude oligonucleotide were dried down and resuspended in 15 mcl of marker dye (90% de-ionised formamide, 10mM tris, 10 mM borate, 1mM EDTA, 0.1% bromophenol blue). The samples were heated at 90° for 1 minute and then loaded onto a 1.2 mm thick denaturing polyacrylamide gel with 1.6 mm wide slots. The gel was prepared from a stock of 15% acrylamide, 0.6% bisacrylamide and 7M urea in 1 X TBE and was polymerised with 0.1% ammonium persulphate and 0.025% TEMED. The gel was pre-run for 1 The samples were run at 1500 V for 4-5 hr. bands were visualised by UV shadowing and those corresponding to the full length product cut out and transferred to micro-testubes. The oligomers were eluted from the gel slice by soaking in AGEB (0.5 M ammonium acetate, 0.01 M magnesium acetate and 0.1 % SDS) overnight. The AGEB buffer was then transferred to fresh tubes and the oligomer precipitated with three volumes of ethanol at -70° for 15 min. The precipitate was collected by centrifugation in an Eppendorf microfuge for 10 min, the pellet washed in 80 % ethanol, the purified oligomer dried, redissolved in 1 ml of water and finally filtered through a 0.45 micron The concentration of purified product micro-filter. was measured by determining its absorbance at 260 nm.

3) Kinasing of oligomers

250 pmole of oligomer was dried down and resuspended in 20 mcl kinase buffer (70 mM Tris pH 7.6, 10 mM $\overline{\text{MgCl}}_2$, 1 mM ATP, 0.2 mM spermidine, 0.5 mM dithiothreitol). 10 u of T4 polynucleotide kinase was added and the mixture incubated at 37° for 30 min. The kinase was then inactivated by heating at 85° for 15 min.

4) Annealing

8 mcl of each oligomer was mixed, heated to 90° and then slow cooled to room temperature over a period of an hour.

5) Ligation

5 mcl of each annealed pair of oligomers were mixed and 10 X ligase buffer added to give a final ligase reaction mixture (50 mM Tris pH 7.5, 10 mM MgCl_2 , 20 mM dithiothreitol, 1 mM ATP. T4 DNA ligase was added at a rate of 100 u per 50 mcl reaction and ligation carried out at 15° for 4 hr.

6) Agarose gel electrophoresis

Ligation products were separated using 2% low gelling temperature agarose gels in 1 X TBE buffer (0.094 M Tris pH 8.3, 0.089 M boric acid, 0.25 mM EDTA) containing 0.5 mcg ml⁻¹ ethidium bromide.

7) Isolation of ligation product

The band corresponding to the expected streptavidin gene ligation product was identified by reference to size markers under long wave UV illumination. The band was cut out of the gel and the DNA extracted as follows.

The volume of the gel slice was estimated from its weight and then melted by incubation at 65° for 10 min. The volume of the slice was then made up to 400 mcl with TE (10 mM Tris pH 8.0, 1 mM EDTA) and Na acetate added to a final concentration of 0.3 M. 10 mcg of yeast tRNA was also added as a carrier. The DNA was then subjected to three rounds of extraction with equal volumes of TE equilibrated phenol followed by three extractions with ether that had been saturated with water. The DNA was precipitated with 2 volumes of ethanol, centrifuged for 10 min in a microfuge, the pellet washed in 70 % ethanol and finally dried down. The DNA was taken up in 20 mcl of TE and 2 mcl run on a 2 % agarose gel to estimate the recovery of DNA.

8) Cloning of fragment

0.5 mcg of pUC18 DNA (eg ATCC 37253) was prepared by cleavage with <u>HindIII</u> and <u>BamHI</u> as advised by the suppliers. The digested DNA was run on an 0.8 % LGT gel and the vector band purified as described above.

20 ng of cut vector DNA was then ligated to various quantities of streptavidin DNA ranging from 2 to 20 ng for 4 hr using the ligation buffer described above.

The ligation products were used to transform competent HW87 as has been described. Ampicillin resistant transformants were selected on L-agar plates containing 100 mcg ml⁻¹ ampicillin.

9) Isolation of plasmid DNA

Plasmid DNA was prepared from the colonies containing potential streptavidin clones essentially as described (Ish-Horowicz, D., Burke, J.F. <u>Nucleic Acids Research</u> 9 2989-2998 (1981).

10) Dideoxy sequencing

The protocol used was essentially as has been described (Biggin, M.D., Gibson, T.J., Hong, G.F. P.N.A.S. 80 3963-3965 (1983)). The method was modified to allow sequencing on plasmid DNA as described (Guo, L-H., Wu, R. Nucleic Acids Research 11 5521-5540 (1983).

11) Transformation

Transformation was accomplished using standard procedures. The strain used as a recipient in the cloning was HW87 which has the following genotype:

araD139(ara-leu)del7697 (lacIPOZY)del74 galU galK hsdR
rpsL srl recA56

Any other standard cloning recipient such as HB101 would be adequate.

CLAIMS

1. DNA coding for streptavidin and having restriction sites for the following enzymes:

EcoRI, NdeI, PstI, SalI, SacI, SnaBI, BspMI, KpnI, FspI, PflMI, DraIII, BalI, BstXI, HpaI, NsiI, SpeI, NheI, BstEII, XbaI, BamHI and HindIII

2. DNA including the following sequence:

ATG GAC CCG TCC AAG GAC TCC AAA GCT CAG GTT TCT
GCA GCC GAA GCT GGT ATC ACT GGC ACC TGG TAT AAC
CAA CTG GGG TCG ACT TTC ATT GTG GAA TCT GCG GTT
GAC GGA GCT CTG ACT GGC ACC TAC GAA TCT GCG GTT
GGT AAC GCA GAA TCC CGC TAC GAA TCT GCG CGT
TAT GAC TCT GCA CCT GCC ACC GAT GGC TCT GGT ACC
GCT CTG GGC TGG ACT GTG GCC ACC GAT GGC TCT GGT ACC
GCT CTG GGC TGG ACT GTG GCC ACC GAT GGC TCT GGC CAA
TAC GTT GGC GAC AGC GCC ACT ACC TGG TCT GGC CAA
TAC GTT GGC GGT GCT GAG GCT ACC GAA GCC AAT GCA
TAC GTT AAC CCT GCC ACC ACC ACC GAA GCC AAT GCA
AAA GTT AAG CCT TCT GCT GCT ACC ACC ACC GAA GCC TTT ACC
AAA GTT AAG CCT TCT GCT GCT ACC ACC CTT GAC
AAA GTT AAG CCT TCT GCT GCT ACC CTT GAC CCT
AAG GAA GCA GCC GTA AAC AAC ACC CCT CTA GAC

- 3. A genetic construct comprising DNA as claimed in claim 1 or 2, or a fragment thereof.
- 4. A construct as claimed in claim 3, wherein the fragment comprises at least 10 nucleotides.

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- 5. A construct as claimed in claim 3, wherein the fragment comprises at least 20 nucleotides.
- 6. A construct as claimed in claim 3, wherein the fragment comprises at least 30 nucleotides.
- 7. A construct as claimed in claim 3, wherein the fragment comprises at least 40 nucleotides.
- 8. A construct as claimed in claim 3, wherein the fragment comprises at least 50 nucleotides.
- 9. A construct as claimed in claim 3, which is a vector.
- 10. A genetic construct as claimed in any one of claims 3 to 9 which is or embodies a chimeric gene composing all or a fragment of DNA according to the first or second aspect fused to any other sequence of DNA so as to result in a sequence capable of encoding a hybrid protein possessing biotin binding activity.
- 11. A process for the preparation of DNA as claimed in claim 1 or 2 or a genetic construct in accordance with claim 3, the process comprising coupling successive nucleotides and/or ligating appropriate oligomers.
- 12. DNA substantially as herein described with reference to Figure 2.

FIGURE 1

AMINO ACID SEQUENCE OF STREPTAVIDIN.

M R K I V V A A I A V S L T T V S I T A
-20 -10

S A S A D P S K D S K A Q V S A A E A G -1 1 10

ITGTWYNQLGSTFIVTAGAD 20 30

G A L T G T Y E S A V G N A E S R Y V L 40 50

T G R Y D S A P A T D G S G T A L G W T 60 70

V A W K N N Y R N A H S A T T W S G Q Y 80 90

V G G A E A R I N T Q W L L T S G T T E 100 110

ANAWKSTLVGHDTFTKVKPS 120 130

A A S I D A A K K A G V N N G N P L D A 140 150

V Q Q 159

Cleavage site after leader sequence indicated by |.

FIGURE 2

SEQUENCE OF SYNTHETIC STREPTAVIDIN GENE AND LIST OF USEFUL RESTRICTION SITES.

			M								A							A	
GAA				GAC					100	AAA	GCI	CAG	GIT	TCI Ps		GCC	GAA	JCT	GGT
Eco	KI.	nae Gra	ኮልረጎ ተ	CTC2	360	S S	Lil	CTC	AGG	יזיויו	CGA(CTO	CAA			œ	CIT	CGA:	CCA
CII	nnu	1		C1G		20	110		30		·	4				50			60
I	T	G	T	W	Y	N	Q	L	G	S	T	F	I	V	T	A	G		D
ATC	ACT	GGC	ACC	IGG	CAT	AAC	CAA	CIG				TTC	ATT	GIG	ACO	GCI	GGI	GOG	GAC
TAG	עכת	~~=	TYCC:	אררי	אַרייַע	ביוויו	ست	CAC		alI		AAG	ממיד	CAC	TGG	ŒΆ	CCA	œc	CIG
TUO	IGA	7		ncc		80	GII.	<u> </u>	90		101	10		<u> </u>		10			120
G	A	L	T	G	T	Y	E	S	A	V	G	N	A	E	S		Y		
		CIG	ACI	GGC	ACC	IAO	GAA'	ICI	GCG	GII	GGL	AAO	GCA	GAA	100		TAC Sna		CIG
	CI	CAC	TY2A	تكك	TCC	ביתע	ىلىك	ACA	~~	ሮልል	CCA'	יארן.	CTT	CIT	AGG				GAC
CCI	<u> </u>	13				40			150			16				70			180
			•																
${f T}$		R	Y	D	S	A	P	A	T	D	G	s 	G	T	A	L	G	W	_
ACI	GGC	ŒI.	TAT	GAC	ICI						GGC		GGI Kpn		GCI	CIG	GGC	IGG	ACT
מבא	ccc.	י. כרא	אידיא	cnc:	ልሮል	رو دو	ccy SDM	CCC T	mc	ረጥል	ന്നു				CCA	GAC	m	AΩ	TGA
ıcr		19				00			210			22				30			240
			-																
V	A	W	K	N		Y	R	N	A	H	S	A	T	T	W	S	G		Y
GIG	GCI	TGG	AAA	AAC	AAC	TAT	Œ!		GCG 'SpI		AGC	GCC	ACI	ACL	IGG	ICI		caa stX	TAC
CAC	YYZA	ACC	गुगुग	באויוי	TTG	ልጥል	GCA				TCG	ŒG	TGA	TGC	ACC	AGA	_		AIG
		25				60			270			28				90			300
													_		_	_	_	_	_
	G			E							W								_
GII	GGC	GG1	GCT	GAG	GCT	CGI.	ATC	AAC	ACI	CAG	ille	CIG	pal	ACA	ill	اعتاد	ACI	ACC	GAA
CAA	.003	CCA	CGA	CTO	ŒA	GCA	TAG	TTC	TGA	GTC	'ACC	GAC	TAA'	TGI	AGG	œ	TGA	IGG	CTT
		31				20			330			34				50			360
											_	_		_				_	_
A	N	A	W	K	S	T	L	V	G	Н	D	T	F	T		V Cuu	K	P	S
GC		iI	TGG	AAA	10.		peI		الحاحا	CAI	CAL.	ACC	111	ACC	w	727.1	MAL	U.	101
œ			ACC	TTT	AGC				CCA	GIA	CTG	TGG	ААА	IGG	TTI	CAA	TTC	GGA	AGA
		37				80			390			40				10			420
_	_		_	-	_	-			_	_				_		_	-	_	
A		S	I	D D	A			K			VIIIX				N M	P	L	CAC	A GCT
	Nhe		ATI	GAT	GCI	لبل	AAL	HH	التالية	احاحا	אונט	MAC	AAL		EII		baI		T3CT
			TAA	CIA	CGA	œ	TTC	TT	ŒI	œ	CAT	TTG	TTC						CGA
		43				40			450						4	70			480

V Q Q * *
GITCAGCAATAATAAGGATCCAAGCIT
BamHI HindIII
CAAGTCGTTATTATTCCTAGGTTCGAA
490 500

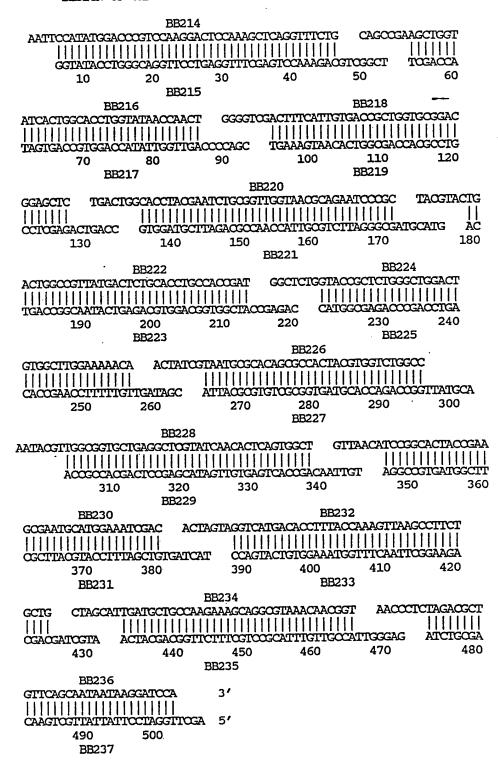
FIGURE 2b

SUMMARY OF USEFUL RESTRICTION SITES.

ENZYME	SEQUENCE	POSITION
EcoRI	= GAATIC	1
NdeI	CATATG	7
PstI	CIGCAG	44
SalI	GIOGAC	90
SacI	GAGCIC	122
SnaBI	TACGIA	172
BspMI.	ACCIGC	201
KpnI	GGIACC	220
FspI	TGCGCA	267
PflMI	CCACTACGIGG	278
DraIII	CACTACGIG	279
BalI .	TGGCCA	291
BstXI	CCAATACGITGG	294
DraIII	CACTCAGIG	327
HpaI	GITAAC	339
NsiI	ATGCAT	365
SpeI	ACTAGT	381
NheI	GCTAGC	424
BSTEII	GGTAACC	463
XbaI	TCTAGA	471
BamHI	GGATCC	496
HinDIII	AAGCIT	502

FIGURE 3

DESIGN OF OLIGOMERS FOR SYNTHETIC STREPTAVIDIN GENE.



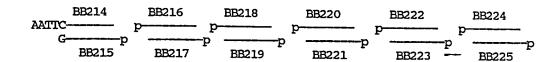
SUBSTITUTE SHEET

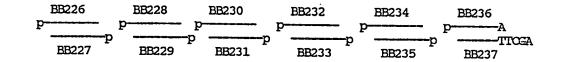
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SUMMARY OF ASSEMBLY PROCEDURE.

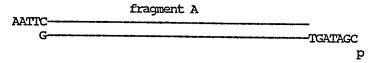
FIGURE 4

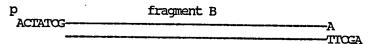
a) kinased oligomers annealed in pairs and mixed in two groups (A & B).





b) oligomers ligated together in two groups. (BB214 and BB237 not kinased to avoid multimerisation.





c) The ligations were checked for the presence of fragment A & B on 2% agarose gels then the ligation reactions were mixed and the reaction allowed to continue to give the final product.

AATTC	-ACTATOGA	
G	TGATAGC	TOGA

d) Streptavidin gene fragment was isolated on a 2% IGT agarose gel and cloned into EcoRI/HinDIII cut pUC18.

		streptavidin	ī	5
vvvvg	AATTC		—A	agcttvvvvv
vvvvcttaa	. G		TTOG/	_
	p			

EcoRI	streptavidin	HinDIII
vvvvgAATTC		Aagcttvvvvv
vvvvcttaaG		TTCGAavvvvv

v = vector sequence

p = 5' phosphates

INTERNATIONAL SEARCH REPORT

International Application No PCT/GB 88/00831

I CLASS	FICATION OF SUBJECT MATTER (it several classific	stion symbols apply, indicate all) *	
According	to International Patent Classification (IPC) or to both Nation	nal Classification and IPC	
IPC ⁴ :	C 12 N 15/00; C 12 P 21/02		
II. FIELDS	SEARCHED		
	Minimum Documenta		
Classificatio	n System C	lassification Symbols	
IPC4	C 12 N; C 12 P		
	Documentation Searched other that to the Extent that such Documents a	an Minimum Documentation are included in the Fields Searched •	
III. DOCU	MENTS CONSIDERED TO BE RELEVANT		1
Category *	Citation of Document, 11 with Indication, where appro	opriate, of the relevant passages 12	Relevant to Claim No. 13
Y	WO, A, 87/05026 (THE TRU UNIVERSITY IN THE CI 27 August 1987 see the whole docume	TY OF NEW YORK)	1-12
Y	WO, A, 86/02077 (BIOGEN 10 April 1986 see the whole docume	1-12	
Y	EP, A, 0171024 (HOECHST 12 February 1986 see page 4, lines 5- lines 7-12	1-12	
Y	WO, A, 83/04053 (APPLIED GENETICS) 24 November see the whole docume	er 1983	1-12
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